

SEQUENCE LISTING

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY5,
EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES

<130> D0041NP/3053-4118US3

<140> TBA

<141> 2001-09-26

<150> 60/235,713

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<151> 2001-01-16

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<170> PatentIn Ver. 2.1

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 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
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Cys Cys Ala Asp Cys Leu Met Gly Val Tyr Leu Phe Phe Val Gly Ile
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Arg Cys Asp Arg Asn Asp Asp Cys Ser Asn Gly Leu Asp Glu Arg Glu
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Cys Asp Ile Tyr Ile Cys Pro Leu Gly Thr His Val Lys Trp His Asn
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His Phe Cys Val Pro Arg Asp Lys Gln Cys Asp Phe Leu Asp Asp Cys
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Arg Cys Asp Ser Val His Asp Cys Val Asp Trp Ser Asp Glu Met Asn		
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450

455

460

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Leu Thr His Leu Asn Leu Ala Asp Asn Asn Ile Thr Ser Leu Lys Asn
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675 680 685

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Val Arg Leu Ile Asp Leu Ser Gly Asn Val Ile Lys Asp Ile Gly Gln

0005533-002501

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930	935	940	
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 Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu
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 Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val
 145 150 155 160
 Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
 165 170 175
 Leu Ser Lys Asn Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly
 180 185 190
 Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu
 195 200 205
 Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp
 210 215 220
 Ile Ser Arg Thr Lys Val His Ser Leu Pro Asn His Gly Leu Glu Asn
 225 230 235 240
 Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Arg Leu Lys Lys Leu Pro
 245 250 255
 Asn Leu Asp Lys Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro
 260 265 270
 Ser His Cys Ala Phe Ala Asn Leu Lys Arg Gln Ile Ser Glu Leu
 275 280 285
 His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Asp Ile Asp Asp Met
 290 295 300
 Thr Gln Ile Gly Asp Gln Arg Val Ser Leu Ile Asp Asp Glu Pro Ser
 305 310 315 320

Leu	His	Glu	Ile	Arg	Ile	Glu	Lys	Ala	Asn	Asn	Leu	Leu	Tyr	Ile	Asn	
			100					105						110		
Pro	Glu	Ala	Phe	Gln	Asn	Leu	Pro	Ser	Leu	Arg	Tyr	Leu	Leu	Ile	Ser	
		115					120					125				
Asn	Thr	Gly	Ile	Lys	His	Leu	Pro	Ala	Val	His	Lys	Ile	Gln	Ser	Leu	
	130					135					140					
Gln	Lys	Val	Leu	Leu	Asp	Ile	Gln	Asp	Asn	Ile	Asn	Ile	His	Ile	Val	
145					150					155					160	
Ala	Arg	Asn	Ser	Phe	Met	Gly	Leu	Ser	Phe	Glu	Trp	Leu	Ser	Lys	Asn	
				165					170					175		
Gly	Ile	Glu	Glu	Ile	His	Asn	Cys	Ala	Phe	Asn	Gly	Thr	Gln	Leu	Asp	
		180						185					190			
Glu	Leu	Asn	Leu	Ser	Asp	Asn	Asn	Asn	Leu	Glu	Glu	Leu	Pro	Asn	Asp	
	195					200						205				
Val	Phe	Gln	Gly	Ala	Ser	Gly	Pro	Val	Ile	Leu	Asp	Ile	Ser	Arg	Thr	
	210					215					220					
Lys	Val	His	Ser	Leu	Pro	Asn	His	Gly	Leu	Glu	Asn	Leu	Lys	Lys	Leu	
225					230					235					240	
Arg	Ala	Arg	Ser	Thr	Tyr	Arg	Trp	Lys	Lys	Leu	Pro	Asn	Leu	Asp	Lys	
				245					250					255		
Phe	Val	Thr	Leu	Met	Glu	Ala	Ser	Leu	Thr	Tyr	Pro	Ser	His	Cys	Cys	
		260						265					270			
Ala	Phe	Ala	Asn	Leu	Lys	Arg	Gln	Ile	Ser	Glu	Leu	His	Pro	Ile	Cys	
	275						280					285				
Asn	Lys	Ser	Ile	Leu	Arg	Gln	Asp	Ile	Asp	Asp	Met	Thr	Gln	Ile	Gly	
	290					295					300					
Asp	Gln	Arg	Val	Ser	Leu	Ile	Asp	Asp	Glu	Pro	Ser	Tyr	Gly	Lys	Gly	
305				310					315						320	
Ser	Asp	Met	Met	Tyr	Asn	Glu	Phe	Asp	Tyr	Asp	Leu	Cys	Asn	Glu	Val	
				325				330						335		
Val	Asp	Val	Thr	Cys	Ser	Pro	Lys	Pro	Asp	Ala	Phe	Asn	Pro	Cys	Gly	
		340						345				350				

Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe
610 615 620

Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly
625 630 635 640

Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Ala
645 650 655

Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser Ser Ala Pro Arg
660 665 670

Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His Ser Ser Gln Asn
675 680 685

<210> 13

<211> 687

<212> PRT

<213> Equus asinus

<400> 13

Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
1 5 10 15

Gly Cys His His Gln Val Cys His Tyr Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Leu Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Lys Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asn Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asp
100 105 110

His Asp Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser

115	120	125
Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu		
130	135	140
Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val		
145	150	155
Glu Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Met Ile Leu Arg		
165	170	175
Leu Ser Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly		
180	185	190
Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu		
195	200	205
Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp		
210	215	220
Ile Ser Gly Thr Arg Ile His Ser Leu Pro Asn Tyr Gly Leu Glu Asn		
225	230	235
Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro		
245	250	255
Ser Leu Glu Lys Phe Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro		
260	265	270
Ser His Cys Cys Ala Phe Ala Asn Trp Arg Gln Gln Thr Ser Glu Leu		
275	280	285
Gln Thr Thr Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Met Thr		
290	295	300
Gln Ala Arg Gly Glu Arg Val Ser Leu Ala Glu Asp Asp Glu Ser Met		
305	310	315
Met Tyr Ser Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp Val		
325	330	335
Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met		
340	345	350
Gly Tyr Asp Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala		
355	360	365
Ile Thr Gly Asn Ile Ile Val Leu Val Ile Leu Ile Thr Ser Gln Tyr		

370

375

380

Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp
385 390 395 400

Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val Asp Ile His
405 410 415

Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala
420 425 430

Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Gly Ser Glu Leu Ser
435 440 445

Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr
450 455 460

His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His Ala Ala Ser
465 470 475 480

Val Met Leu Val Gly Trp Ile Phe Gly Phe Gly Val Gly Leu Leu Pro
485 490 495

Ile Phe Gly Ile Ser Thr Tyr Met Lys Val Ser Ile Cys Leu Pro Met
500 505 510

Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val
515 520 525

Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Thr His Ile
530 535 540

Tyr Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Ser Asp Thr
545 550 555 560

Lys Ile Ala Lys Arg Met Gly Ile Leu Ile Phe Thr Asp Phe Leu Cys
565 570 575

Met Ala Pro Ile Ser Phe Phe Gly Ile Ser Ala Ser Leu Lys Val Ala
580 585 590

Leu Ile Thr Val Ser Lys Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro
595 600 605

Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn
610 615 620

Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly Cys Tyr Glu

625 630 635 640
 Met Gln Ala Gln Thr Tyr Arg Thr Glu Thr Ser Ser Thr Gly His Ile
 645 650 655
 Ser His Pro Lys Asn Gly Pro Cys Pro Pro Thr Pro Arg Val Thr Asn
 660 665 670
 Gly Ala Asn Cys Thr Leu Val Pro Leu Ser His Leu Ala Gln Asn
 675 680 685

 <210> 14
 <211> 693
 <212> PRT
 <213> CHICKEN

 <400> 14
 Met Ser Leu Gly Leu Thr Cys Leu Leu Ile Leu Leu Ala Ser Cys Ser
 1 5 10 15
 Gly Cys Gln His His Thr Cys Leu Cys Glu Gly Arg Ile Phe Ile Cys
 20 25 30
 Gln Glu Ile Lys Val Val Gln Leu Pro Arg Asp Ile Pro Thr Asn Ala
 35 40 45
 Thr Glu Leu Arg Phe Val Leu Thr Lys Met Arg Val Ile Pro Lys Gly
 50 55 60
 Ala Phe Thr Gly Leu His Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
 65 70 75 80
 Asp Ala Leu Glu Ile Ile Glu Gly Asn Val Phe Ser Ser Leu Pro Lys
 85 90 95
 Leu His Glu Ile Arg Ile Glu Lys Ala Asn Lys Leu Met Lys Ile Asp
 100 105 110
 Gln Asp Ala Phe Gln His Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser
 115 120 125
 Asn Thr Gly Leu Ser Phe Leu Pro Val Val His Lys Val His Ser Phe
 130 135 140
 Gln Lys Val Leu Leu Asp Val Gln Asp Asn Ile His Ile Arg Thr Ile
 145 150 155 160

Glu Arg Asn Thr Phe Met Gly Leu Ser Ser Glu Ser Val Ile Leu Arg
165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile Lys Asp His Ala Phe Asn Gly
180 185 190

Thr Cys Leu Asp Glu Leu Asn Leu Ser Asp Asn Tyr Asn Leu Glu Lys
195 200 205

Leu Pro Glu Lys Val Phe Gln Gly Ala Ile Gly Pro Val Val Leu Asp
210 215 220

Ile Ser Arg Thr Arg Ile Ser Phe Leu Pro Ser His Gly Leu Glu Phe
225 230 235 240

Ile Lys Lys Leu Arg Ala Arg Ser Thr Tyr Lys Leu Lys Lys Leu Pro
245 250 255

Asp Val Asn Lys Phe Arg Ser Leu Ile Glu Ala Asn Phe Thr Tyr Pro
260 265 270

Ser His Cys Cys Ala Phe Thr Asn Arg Lys Thr Gln Asn Thr Glu Phe
275 280 285

Tyr Pro Ile Cys Ser Met Ser Pro Ala Lys Gln Asp Leu Gly Glu Gln
290 295 300

Thr Gly Lys Arg Lys His Arg Arg Ser Ala Ala Glu Asp Tyr Ile Ser
305 310 315 320

His Tyr Gly Thr Arg Phe Gly Pro Val Glu Asn Glu Phe Asp Tyr Gly
325 330 335

Leu Cys Asn Glu Val Val Asp Phe Val Cys Ser Pro Lys Pro Asp Ala
340 345 350

Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Val Leu Arg Val Leu
355 360 365

Ile Trp Phe Ile Asn Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu
370 375 380

Ile Ile Leu Ile Ser Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu
385 390 395 400

Met Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu
405 410 415

Pro Thr Ala Ser Lys Asn Ser Asp Gly Thr Ile Tyr Ser Leu Val Pro
675 680 685

Leu Asn His Leu Asn
690

<210> 15

<211> 676

<212> PRT

<213> Callithrix jacchus

<400> 15

Met Lys Gln Pro Leu Leu Ala Leu Gln Leu Leu Lys Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Pro Leu Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Arg
20 25 30

Cys Cys Pro Glu Pro Cys Asn Cys Thr Pro Asp Gly Ala Leu Arg Cys
35 40 45

Pro Gly Pro Gly Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro
50 55 60

Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile
65 70 75 80

Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn
85 90 95

Ala Phe Asp Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr
100 105 110

Lys Asn Leu Ile His Ile Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg
115 120 125

Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp
130 135 140

Val Thr Lys Ile Phe Ser Ser Glu Thr Asn Phe Ile Leu Glu Ile Cys
145 150 155 160

Asp Asn Leu His Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met
165 170 175

Asn Asn Glu Ser Ile Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu
180 185 190

Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met
450 455 460

Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val
465 470 475 480

Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met His Ile
485 490 495

Glu Thr Pro Phe Ser Gln Ala Tyr Val Ile Phe Leu Leu Val Leu Asn
500 505 510

Val Leu Ala Phe Val Ile Ile Cys Ile Cys Tyr Ile Cys Ile Tyr Phe
515 520 525

Thr Val Arg Asn Pro Asn Val Ile Ser Ser Asn Ser Asp Thr Lys Ile
530 535 540

Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala
545 550 555 560

Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Met Pro Leu Ile
565 570 575

Thr Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn
580 585 590

Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Arg
595 600 605

Arg Asp Phe Phe Leu Leu Leu Gly Lys Phe Gly Cys Cys Lys His Arg
610 615 620

Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Tyr
625 630 635 640

Lys Asn Gly Phe Thr Gly Ser Ser Lys Pro Ser Gln Ser Thr Leu Lys
645 650 655

Leu Pro Ala Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Cys
660 665 670

Tyr Lys Glu Tyr
675

<210> 16

<211> 907
 <212> PRT
 <213> HUMAN

<400> 16

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
 1 5 10 15

Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
 20 25 30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
 35 40 45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
 50 55 60

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
 65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
 85 90 95

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
 100 105 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
 115 120 125

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
 130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
 145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
 165 170 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
 180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
 195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
 210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp

225 230 235 240
 Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
 245 250 255
 Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270
 Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
 275 280 285
 Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
 290 295 300
 Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
 305 310 315 320
 Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
 325 330 335
 Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350
 Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365
 Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380
 Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
 385 390 395 400
 Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415
 Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
 420 425 430
 Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
 435 440 445
 Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
 450 455 460
 Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
 465 470 475 480
 Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn

485	490	495
Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly		
500	505	510
Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp		
515	520	525
Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser		
530	535	540
Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile		
545	550	555
Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala		
565	570	575
Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile		
580	585	590
Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val		
595	600	605
Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe		
610	615	620
Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile		
625	630	635
Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr		
645	650	655
Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe		
660	665	670
Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys		
675	680	685
Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser		
690	695	700
Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro		
705	710	715
Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys		
725	730	735
Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp		

740

745

750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
865 870 875 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

<210> 17

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 17

Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys
1 5 10 15

<210> 18

<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 18
Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met
1 5 10 15

Glu Ser Val Gln Cys Arg
20

<210> 19
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 19
Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly
1 5 10 15

Lys Arg Gln Thr Ser
20

<210> 20
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 20
Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
1 5 10 15

Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser
20 25 30

<210> 21

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21

Ser	Ile	Gln	Lys	Thr	Ala	Leu	Gln	Thr	Thr	Glu	Val	Arg	Asn	Cys	Phe
1				5				10					15		

Gly	Arg	Glu	Val	Ala	Val	Ala	Asn	Arg
		20					25	

<210> 22

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22

Arg	Val	Glu	Ile	Pro	Asp	Thr	Met	Thr	Ser	Trp
1				5				10		

<210> 23

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23

Thr	Asn	Phe	Phe	Lys	Asp	Lys	Leu	Lys	Gln	Leu	Leu	His	Lys	His	Gln
1				5				10				15			

Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile
 20 25 30

Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys
 35 40 45

Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val Ser
 50 55 60

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GPCR21-F1
 forward primer

<400> 24
 tgtgttaagg ccacgctgtt ag 22

<210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GPCR21-R1
 reverse primer

<400> 25
 tcactgtgat ggcaaggatg a 21

<210> 26
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GAPDH-F3
 forward primer

<400> 26
 agccgagcca catcgct 17

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 27

gtgaccaggc gcccaatac

19

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 28

caaatccggt gactccgacc ttcacctt

28

<210> 29
<211> 99
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 1;
N=A+G+C+T; K=C+G+T

<400> 29

cgaagcgtaa gggcccagcc ggccnnknkn nnknknknkn nknnknknkn knknknknkn 60
nnknknknkn nknnknknkn knnkcgggt ccggcgggc 99

<210> 30
<211> 95
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 2;
N=A+G+C+T; V=C+A+G

<400> 30
aaaaggaaaa aagcgggcgc vnnvnnvnnv nnvnnvnnvn nnvnnvnnvn vnnvnnvnnv 60
nnvnnvnnvn nnvnnvnnvn gccgcccggg cccgg 95

<210> 31
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 31
Pro Gly Pro Gly Gly
1 5

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 32
Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys Ile His
1 5 10

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33
Cys Ile Arg His Ile Ser Arg Lys Ala Phe Phe Gly Leu
1 5 10

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34
His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys
1 5 10

<210> 35
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35
Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu
1 5 10

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36
Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu
1 5 10

<210> 37
<211> 13
<212> PRT
<213> Artificial Sequence

Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp
1 5 10

<210> 41

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41

Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys
1 5 10

<210> 42

<211> 14

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu
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<210> 43

<211> 14

<212> PRT

<213> Artificial Sequence

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polypeptide

<400> 43

Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn
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<210> 44

<211> 14

<400> 47

Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile
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<210> 48

<211> 14

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polypeptide

<400> 48

Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala
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<210> 49

<211> 14

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polypeptide

<400> 49

Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys
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<210> 50

<211> 14

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 50

Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser
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<210> 51
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polypeptide

<400> 51
Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr
1 5 10

<210> 52
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polypeptide

<400> 52
Pro Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys Asn
1 5 10

<210> 53
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<400> 53
Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys
1 5 10

<210> 54
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<212> PRT
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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala
1 5 10 15

<210> 55

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala Leu Thr Gln Glu
1 5 10 15

<210> 56

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56

Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
1 5 10 15

<210> 57

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57

Ile Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe
1 5 10 15

<210> 58
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<223> Description of Artificial Sequence: Synthetic 5'
primer

<400> 58
gcagcagcgg ccgcagaata ttgtctggg ttatagc

37

<210> 59
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<212> DNA
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<220>

<223> Description of Artificial Sequence: Synthetic 3'
primer

<400> 59
gcagcagtcg acggaaactg gtttcattat actgtc

36

<210> 60
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic 5'
primer

<400> 60
gcagcagcgg ccgcagtggtc ttctacttc atttcacg

39

<210> 61
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic 3'

primer

<400> 61

gcagcagtcg acggttggtga gagtatagag cattgg

36